



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/042,894  
Source: 01DE  
Date Processed by STIC: 1/29/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efsc/efs/downloads/documents.htm>>, EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 101042,894

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (3) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (x3) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>      Sequence(s) 26-28 missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of a      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIEP

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
 TIME: 14:44:47

Input Set : A:\seqlist.txt  
 Output Set: N:\CRF3\01272002\J042894.raw

Does Not Comply  
 Corrected Diskette Needed

10 <110> APPLICANT: Shi, Jinrui  
 5 Beach, Larry  
 6 Wang, Hongyu  
 7 Rafalski, Antoni J.  
 8 Rebecca E. Cahoon  
 10 <120> TITLE OF INVENTION: Novel Inositol Polyphosphate Kinase  
 11 Genes and Uses Thereof  
 13 <130> FILE REFERENCE: 1286  
 15 <140> CURRENT APPLICATION NUMBER: US/10/042,894  
 15 <141> CURRENT FILING DATE: 2002-01-09  
 15 <150> PRIOR APPLICATION NUMBER: US 60/261,465  
 16 <151> PRIOR FILING DATE: 2001-01-12  
 18 <160> NUMBER OF SEQ ID NOS: 37  
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0

*cross  
 throughout*

# ERRORED SEQUENCES

104 <210> SEQ ID NO: 2  
 105 <211> LENGTH: 240  
 106 <212> TYPE: PRT  
 107 <213> ORGANISM: Zea mays  
 109 <400> SEQUENCE: 2  
 110 Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala  
 111 1 5 10 15  
 112 Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr  
 113 20 25 30  
 114 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr  
 115 35 40 45  
 116 Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr  
 117 50 55 60  
 118 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln  
 119 65 70 75 80  
 120 Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly  
 121 85 90 95  
 122 Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp  
 123 100 105 110  
 124 Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Tyr Leu Ala Lys Asp  
 125 115 120 125  
 126 Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Leu Arg Pro Ser  
 127 130 135 140  
 128 Arg Arg Pro Arg Gly Arg Val Ala Asp Gly Ala Pro Gly Gly Glu  
 129 145 150 155 160

*p2*

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
 TIME: 14:44:47

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\01272002\J042894.raw

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130 Gly Tyr Gly His Arg Arg Arg Pro Pro Arg Ala Pro Ala Leu Arg Val
131                               165                               170                               175
132 Ile Arg Leu Pro Thr Arg Gly Trp Thr Ala Arg Ser Arg Arg Arg Cys
133                               180                               185                               190
134 Thr Glu Glu Lys Val Glu Ser Cys His Ser Cys Ala Ser Ser Arg His
135                               195                               200                               205
136 Gly Trp Arg Ser Arg Leu Cys Ser Thr Ser Thr Arg Arg Arg Phe Phe
E--> 137
      210                               215                               220
217 <210> SEQ ID NO: 4
218 <211> LENGTH: 227
219 <212> TYPE: PRT
220 <213> ORGANISM: Zea mays
222 <400> SEQUENCE: 4
223 Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala
224 1                               5                               10                               15
225 Ser Ala Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr
226                               20                               25                               30
227 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
228                               35                               40                               45
229 Glu Ala Phe Ser Ala His Ala Val Pro Ala Arg Ile Arg Asp Thr
230 50                               55                               60
231 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
232 65                               70                               75                               80
233 Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
234                               85                               90                               95
235 Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp
236                               100                              105                              110
237 Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp
238                               115                              120                              125
239 Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg
240 130                              135                              140
241 Val Val Val Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val
242 145                              150                              155                              160
243 Lys Ala Met Asp Thr Val Gly Val Arg Arg Val Leu Arg Arg Tyr Val
244                               165                               170                               175
245 Ser Ser Ala Cys Arg Arg Gly Asp Gly Leu Arg Ala Arg Gly Gly Gly
246                               180                               185                               190
247 Val Arg Arg Lys Arg Trp Ser Leu Val Thr Ala Ala Arg Ala Gln Gly
E--> 248
      195                               200                               205
338 <210> SEQ ID NO: 6
339 <211> LENGTH: 289
340 <212> TYPE: PRT
341 <213> ORGANISM: Zea mays
343 <400> SEQUENCE: 6
344 Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala
345 1                               5                               10                               15
346 Ser Ala Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr
347                               20                               25                               30
348 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr

```

*↑ Trp Ala Met Met Leu Leu Gln Ser  
insert hard return*

*↑ Val Val Arg Gly Ala Ala Ser Val  
insert hard return*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
TIME: 14:44:47

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\01272002\J042894.raw

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349          35          40          45
350 Glu Ala Phe Ser Ala His Ala Val Pro Ala Arg Ile Arg Asp Thr
351      50          55          60
352 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
353 65          70          75          80
354 Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
355      85          90          95
356 Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp
357      100          105          110
358 Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp
359      115          120          125
360 Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg
361      130          135          140
362 Val Val Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val
363 145          150          155          160
364 Lys Ala Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val
365      165          170          175
366 Ser Ser Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Val
367      180          185          190
368 Tyr Gly Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala
369      195          200          205
370 Trp Phe Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu
371      210          215          220
372 Leu Gly Tyr Asp Ala Ala Ala Val Ala Ala Gly Gly Gly Gly Gly
373 225          230          235          240
374 Val Thr Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly
375      245          250          255
376 Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe
E--> 377
          260          265          270
474 <210> SEQ ID NO: 8
475 <211> LENGTH: 289
476 <212> TYPE: PRT
477 <213> ORGANISM: Zea mays
479 <400> SEQUENCE: 8
480 Met Ser Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala
481 1          5          10          15
482 Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr
483      20          25          30
484 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
485      35          40          45
486 Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
487      50          55          60
488 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
489 65          70          75          80
490 Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
491      85          90          95
492 Phe Gln Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp
493      100          105          110
494 Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Lys Asp

```

↑ Val Ser Asp Ile Val Pro Glu Thr  
Insert hard return

RAW SEQUENCE LISTING  
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Output Set: N:\CRF3\01272002\J042894.raw

```

495          115          120          125
496 Arg Gly Thr Thr Ser Val Leu Gly Phe Arg Val Ser Gly Val Arg
497          130          135          140
498 Val Val Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val
499 145          150          155          160
500 Lys Ala Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val
501          165          170          175
502 Ser Ser Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Val
503          180          185          190
504 Tyr Gly Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala
505          195          200          205
506 Trp Phe Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu
507          210          215          220
508 Leu Gly Tyr Asp Ala Ala Val Ala Ala Gly Gly Asp Gly Gly Gly
509 225          230          235          240
510 Val Thr Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly
511          245          250          255
512 Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe
E--> 513

          260          265          270          ↑ Val Ser Asp Ile Val Pro Glu Thr
602 <210> SEQ ID NO: 10
603 <211> LENGTH: 279
604 <212> TYPE: PRT
605 <213> ORGANISM: Glycine max
607 <400> SEQUENCE: 10
608 Met Leu Lys Ile Pro Glu His Gln Val Ala Gly His Lys Ala Lys Asp
609 1          5          10          15
610 Gly Ile Leu Gly Pro Leu Val Asp Asp Phe Gly Lys Phe Tyr Lys Pro
611          20          25          30
612 Leu Gln Thr Asn Lys Asp Asp Asp Thr Arg Gly Ser Thr Glu Leu Ser
613          35          40          45
614 Phe Tyr Thr Ser Leu Ala Ala Ala His Asp Tyr Ser Ile Arg Ser
615          50          55          60
616 Phe Phe Pro Ala Phe His Gly Thr Arg Leu Leu Asp Ala Ser Asp Gly
617 65          70          75          80
618 Ser Gly Pro His Pro His Leu Val Leu Glu Asp Leu Leu Cys Gly Tyr
619          85          90          95
620 Ser Lys Pro Ser Val Met Asp Val Lys Ile Gly Ser Arg Thr Trp His
621          100          105          110
622 Leu Gly Asp Ser Glu Asp Tyr Ile Cys Lys Cys Leu Lys Lys Asp Arg
623          115          120          125
624 Glu Ser Ser Ser Leu Pro Leu Gly Phe Arg Ile Ser Gly Val Lys Asp
625          130          135          140
626 Ser Ile Ser Ser Trp Glu Pro Thr Arg Lys Ser Leu Gln Cys Leu Ser
627 145          150          155          160
628 Ala His Gly Val Ala Leu Val Leu Asn Lys Phe Val Ser Ser Asn Asn
629          165          170          175
630 Ile Asn His Asp Asp His His Pro Asp Cys Ala Phe Ala Thr Glu Val
631          180          185          190
632 Tyr Gly Ala Val Leu Glu Arg Leu Gln Lys Leu Lys Asp Trp Phe Glu

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*hard return*

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```

633          195          200          205
634 Val Gln Thr Val Tyr His Phe Tyr Ser Cys Ser Val Leu Val Val Tyr
635          210          215          220
636 Glu Lys Asp Leu Gly Lys Gly Lys Ala Thr Asn Pro Leu Val Lys Leu
637 225          230          235          240
638 Val Asp Phe Ala His Val Val Asp Gly Asn Gly Val Ile Asp His Asn
E--> 639
          245          250          255
739 <210> SEQ ID NO: 12
740 <211> LENGTH: 310
741 <212> TYPE: PRT
742 <213> ORGANISM: Eucalyptus grandis
744 <400> SEQUENCE: 12
745 Met Leu Lys Val Pro Asp His Gln Val Ala Gly His Arg Gly Asp Gly
746 1          5          10          15
747 Gly Lys Leu Gly Pro Leu Val Asp Asp Ser Gly Arg Phe Tyr Lys Pro
748          20          25          30
749 Leu Gln Ser Asp His Arg Gly Asp Thr Glu Val Ala Phe Tyr Glu Ser
750          35          40          45
751 Phe Tyr Ser Asn Thr Glu Ile Pro Gly His Ile Arg Lys Phe Phe Pro
752 50          55          60
753 Ala Phe His Gly Thr Lys Thr Ile Glu Ala Ser Asp Gly Ser Gly Pro
754 65          70          75          80
755 Gln Pro His Leu Val Leu Glu Asp Leu Val Ser Gly Arg Thr Asn Pro
756          85          90          95
757 Ser Leu Met Asp Ile Lys Thr Gly Ser Arg Thr Trp Tyr Pro Glu Ala
758          100          105          110
759 Ser Glu Glu Tyr Ile Gln Lys Cys Leu Glu Lys Asp Arg Asn Ser Thr
760          115          120          125
761 Ser Val Ser Leu Gly Phe Arg Ile Ser Gly Leu Arg Val Tyr Gln Asn
762          130          135          140
763 Ser Glu Ala Gly Phe Trp Gln Pro Glu Lys Lys Val Val Tyr Ser Phe
764 145          150          155          160
765 Asn Ala Asp Gly Val Arg Ser Ala Leu Arg Lys Phe Val Ser Ser Asn
766          165          170          175
767 Leu Ser Leu Gly Pro Asn Val Asp Pro Asp Cys Leu Tyr Ala Ser Lys
768          180          185          190
769 Val Tyr Cys His Arg Gly Gly Ile Leu Ala Gln Leu Leu Gln Leu Lys
770          195          200          205
771 Glu Trp Phe Glu Val Gln Thr Asn Tyr His Phe Tyr Ser Cys Ser Leu
772          210          215          220
773 Ile Ile Leu Tyr Asp Arg Glu Ser Ala Leu Asp Gly Cys Ala His Pro
774 225          230          235          240
775 Lys Val Lys Leu Val Asp Phe Ala His Val Met Asp Gly His Gly Val
776          245          250          255
777 Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Val Ile Lys Phe Ile
778          260          265          270
779 Arg Asp Ile Ala Asp Glu Asp Asn Lys Cys Ala Lys Cys Glu Val Asn
E--> 780
          275          280          285
871 <210> SEQ ID NO: 14
          ↑
          Leu Gly Leu Lys Glu Asn Gly Phe
          hard return

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
 TIME: 14:44:47

Input Set : A:\seqlist.txt  
 Output Set: N:\CRF3\01272002\J042894.raw

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872 <211> LENGTH: 295
873 <212> TYPE: PRT
874 <213> ORGANISM: Parthenium argentatum
876 <400> SEQUENCE: 14
877 Met Leu Lys Ala Pro Asp His Gln Val Ala Gly His Glu Ala Gly Leu
878 1 5 10 15
879 Gly Lys Leu Gly Pro Leu Ile Asp Ser Ser Gly Arg Phe Tyr Lys Pro
880 20 25 30
881 Leu Gln Gly Asp Asn Arg Gly Ser Glu Glu Val Ala Phe Tyr Glu Ser
882 35 40 45
883 Phe Ser Ser Asn Asn Asn Ile Pro Glu His Ile Arg Lys Phe Phe Pro
884 50 55 60
885 Ile Tyr Tyr Gly Thr Lys Ile Met Lys Ala Ser Thr Gly Ser Asp His
886 65 70 75 80
887 Pro His Met Val Leu Gln Asp Leu Thr Ser Ala His Val Asn Pro Ser
888 85 90 95
889 Val Met Asp Ile Lys Ile Gly Ser Arg Thr Trp Ala Pro Glu Ala Ser
890 100 105 110
891 Glu Ala Tyr Ile Ala Lys Cys Leu Lys Lys Asp Arg Glu Ser Thr Ser
892 115 120 125
893 Ile Pro Leu Gly Phe Arg Ile Ser Gly Leu Gln Val Tyr Ile Asp Asp
894 130 135 140
895 Gly Ser Gly Phe Tyr Lys Pro His Arg Asn Tyr Met Arg Lys Thr Gly
896 145 150 155 160
897 Pro Ala Asp Val Arg Leu Leu Leu Arg Lys Phe Val Ser Ser Asn Pro
898 165 170 175
899 Ser Ala Glu Met Glu Met Arg Thr Gly Leu Gly Pro Asp Cys Ser Leu
900 180 185 190
901 Ala Ser Phe Val Tyr Gly Gly Pro Asn Gly Ile Leu Ala Gln Leu Met
902 195 200 205
903 Glu Leu Lys Thr Trp Phe Glu Asp Gln Thr Ile Tyr His Phe Tyr Ala
904 210 215 220
905 Cys Ser Phe Leu Phe Ile Phe Glu Lys Arg Leu Val Leu Lys Gly Ala
906 225 230 235 240
907 Arg Ser Asn Ala Glu Val Lys Leu Ile Asp Phe Ala His Val Thr Asp
908 245 250 255
909 Gly Asn Gly Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu

```

E--> 910

```

          260          265          270          ↑ Ile Lys Phe Ile Ser Asp Ile Leu
964 <210> SEQ ID NO: 16
965 <211> LENGTH: 111
966 <212> TYPE: PRT
967 <213> ORGANISM: Zea mays
969 <400> SEQUENCE: 16
970 Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala
971 1 5 10 15
972 Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr
973 20 25 30
974 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
975 35 40 45

```

*hard return*



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Input Set : A:\seqlist.txt

Output Set: N:\CRF3\01272002\J042894.raw

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976 Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
977 50 55 60
978 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
979 65 70 75 80
E--> 980
Pro Gly Glu Pro His Pro Tyr Leu Val Leu Asp Asp Leu Leu Ala Gly 85
982 <210> SEQ ID NO: 17
983 <211> LENGTH: 643
984 <212> TYPE: DNA
985 <213> ORGANISM: Zea mays
987 <220> FEATURE:
988 <221> NAME/KEY: misc_feature
989 <222> LOCATION: (1)...(643)
990 <223> OTHER INFORMATION: n = A,T,C or G
992 <400> SEQUENCE: 17
W--> 993 ggcgcgtccct gntttttgtta accaccccgcc cccaaaatct cttttccgcg tgcgctgcga 60
994 accaccgctc tccaccatcg ccaactcgta ccccttgctc ccatagtcgc cataccatgc 120
995 ccgaactcca ccgcgcggag caccgaagtcg ccggtcaccg cgctccgcgc agcaagctgg 180
996 gcccgctcat cgacggtccc ggcctcttct acaagccgct ccaggccggc gaccgtgggg 240
W--> 997 agcacagggt cgccttctat gaggcgttct cgcgccacgc cgcgtcccg gcccgcatcc 300
998 gagacacott cttccccgcg ttccacggca cgcgactcct ccccaaccg gcgcagcccg 360
999 gggagccgca tcgcacacct gtctcgacg acctcctcgc ggggtttgag gcgccttcg 420
1000 tcgcagacat caagatcgcc gccatcacgt ggccaccgag ttgcgcggag cctcatcg 480
E--> 1001
ncaagtacct ngccaaaggac cgcggggaca cgagcgttct gctcggattc cgcgtcttgc 540gtccgagtcg tcggcccccga
1003 <210> SEQ ID NO: 18
1004 <211> LENGTH: 519
1005 <212> TYPE: DNA
1006 <213> ORGANISM: Zea mays
1008 <220> FEATURE:
1009 <221> NAME/KEY: misc_feature
1010 <222> LOCATION: (1)...(519)
1011 <223> OTHER INFORMATION: n = A,T,C or G
1013 <400> SEQUENCE: 18
W--> 1014 ggtacggang aaaangtgga gtcttgtcac agctgcgcga gctcaangcg tggttcgagg 60
1015 ggcagactct gtccacttc tactcgcgct cgattctctt gggctatgat gctgtgcgag 120
W--> 1016 tcgcagcagc cggangtggg ggtggggtaa cagtgaagct ggtggacttt gcccatgtgg 180
W--> 1017 ccgagggtga tgggggtgatt gaccacaact tctcggcgcg gctctgctan ctgataaagt 240
1018 ttgtttctga cattgttcca gagactctcc agacgcagcc ttgggtcctc tcttaagaaa 300
W--> 1019 agatctctggc attttcgatt tgataacaaa ggaanacatt tcagctgcga aaaaaaaanc 360
E--> 1020
accagtgaag atgaaaataa cattattgag gaaagttccg atnataaccc accanattna 420gtaaaaaaa gtcccaaat
1022 <210> SEQ ID NO: 19
1023 <211> LENGTH: 353
1024 <212> TYPE: DNA
1025 <213> ORGANISM: Zea mays
1027 <220> FEATURE:
1028 <221> NAME/KEY: misc_feature
1029 <222> LOCATION: (1)...(353)
1030 <223> OTHER INFORMATION: n = A,T,C or G
1032 <400> SEQUENCE: 19
1033 ctcaaggcat ggttgaggga gcagactctg ttccacttct actcggcgtc gattctctg 60

```

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
 TIME: 14:44:47

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\01272002\J042894.raw

W--> 1034 ggctatgatg ctgctgcagt cgcancaggc ggaggtgggg gtggggtaac agtgaagctg 120  
 1035 gtggactttg cccatgtggc cgaggggtgat ggggttgatt tgaccacaac ttctctggcg 180

E--> 1036  
 agctctgcta gctgatcaag ttccgtttct tgacattggt ccaganaactc cttagacgcc 240agcctttggg tccttecta  
 1132 <210> SEQ ID NO: 21  
 1133 <211> LENGTH: 111  
 1134 <212> TYPE: PRT  
 1135 <213> ORGANISM: Zea mays  
 1137 <400> SEQUENCE: 21  
 1138 Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala  
 1139 1 5 10 15  
 1140 Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly Leu Phe Tyr  
 1141 20 25 30  
 1142 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr  
 1143 35 40 45  
 1144 Glu Ala Phe Ser Ala His Ala Val Pro Ala Arg Ile Arg Asp Thr  
 1145 50 55 60  
 1146 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln  
 1147 65 70 75 80

E--> 1148  
 Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly ↑ 85  
 1256 <210> SEQ ID NO: 23  
 1257 <211> LENGTH: 322  
 1258 <212> TYPE: PRT  
 1259 <213> ORGANISM: Parthenium argentatum  
 1261 <400> SEQUENCE: 23  
 1262 Met Leu Pro Ala Pro Ala Val Pro Asn Gly Thr Gly Ala Pro Leu Lys  
 1263 1 5 10 15  
 1264 Asp Glu Pro Ser Asn Pro Asp Gln Ala Gln His Gln Pro Asp Glu Arg  
 1265 20 25 30  
 1266 Val Gln His Phe Ile Leu Leu Glu Asp Leu Thr Ala Gly Met Thr Arg  
 1267 35 40 45  
 1268 Pro Cys Val Leu Asp Leu Lys Met Gly Thr Arg Gln Tyr Gly Val Glu  
 1269 50 55 60  
 1270 Ala Asp Glu Lys Lys Gln Arg Ser Gln Arg Arg Lys Cys Gln Met Thr  
 1271 65 70 75 80  
 1272 Thr Ser Ala Gln Leu Gly Val Arg Val Cys Gly Met Gln Ile Trp Asn  
 1273 85 90 95  
 1274 Ala Lys Thr Gln Ser Tyr Ile Phe Glu Asp Lys Tyr Phe Gly Arg Asp  
 1275 100 105 110  
 1276 Leu Lys Ala Gly Lys Glu Phe Gln Asp Ala Leu Lys Arg Phe Phe Trp  
 1277 115 120 125  
 1278 Asp Gly Thr Ser Tyr Lys Ala Ala Asn Arg His Ile Pro Val Ile Leu  
 1279 130 135 140  
 1280 Glu Lys Ile Ser Gln Leu Glu Arg Met Ile Arg Lys Leu Pro Gly Tyr  
 1281 145 150 155 160  
 1282 Arg Phe Tyr Ala Ser Ser Leu Leu Met Leu Tyr Asp Arg Gly Asp Gly  
 1283 165 170 175  
 1284 Glu Ser Lys Glu Lys Asp Ala Ala Pro Ser Leu Pro Asn Gly Leu Ser  
 1285 180 185 190  
 1286 Asn Pro Ser Asn Glu Asp Val Ser Thr Ile Pro Ser Gly Leu Thr Ser

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
 TIME: 14:44:47

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\01272002\J042894.raw

```

1287          195          200          205
1288 Pro Gly Pro Thr Val Ala Ser Lys Pro Ser Pro Lys Lys His Gly Glu
1289      210          215          220
1290 Ile Lys Leu Lys Ile Val Asp Phe Ala Asn Cys Val Thr Ala Glu Asp
1291 225          230          235          240
1292 Pro Leu Pro Asp Asp Leu Pro Cys Pro Pro Glu Asn Pro Asp Gly Ile
1293          245          250          255
1294 Asp Arg Gly Tyr Leu Arg Gly Leu Arg Ser Leu Arg Leu Tyr Phe Gln
1295          260          265          270
1296 Arg Ile Trp Asn Asp Ile Asn Glu Glu Trp Val Glu Arg Gly Glu Gly
1297          275          280          285
1298 Glu Gly Met Ala Arg Asn His His Gly Pro Gly Leu Gly Glu Val
E--> 1299
      290          295          300
1414 <210> SEQ ID NO: 25
1415 <211> LENGTH: 316
1416 <212> TYPE: PRT
1417 <213> ORGANISM: Zea mays
1419 <400> SEQUENCE: 25
1420 Thr Arg Pro Arg Lys Leu Arg Asn Ile Val Gln Trp Thr Pro Phe Phe
1421 1      5      10      15
1422 Gln Thr Tyr Lys Lys Gln Arg Tyr Pro Trp Val Gln Leu Ala Gly His
1423      20      25      30
1424 Gln Gly Asn Phe Lys Ala Gly Pro Glu Pro Gly Thr Ile Leu Lys Lys
1425      35      40      45
1426 Leu Cys Pro Lys Glu Gln Leu Cys Phe Gln Val Leu Met Lys Asp Val
1427      50      55      60
1428 Leu Arg Pro Tyr Val Pro Glu Tyr Lys Gly His Leu Thr Thr Asp Asp
1429 65      70      75      80
1430 Gly Asp Leu Tyr Leu Gln Leu Glu Asp Leu Leu Gly Asp Phe Thr Ser
1431      85      90      95
1432 Pro Cys Val Met Asp Cys Lys Ile Gly Val Arg Thr Tyr Leu Glu Glu
1433      100      105      110
1434 Glu Leu Ala Lys Ala Lys Glu Lys Pro Lys Leu Arg Lys Asp Met Tyr
1435      115      120      125
1436 Glu Lys Met Ile Gln Ile Asp Pro Asn Ala Pro Ser Glu Glu Glu His
1437      130      135      140
1438 Arg Leu Lys Gly Val Thr Lys Pro Arg Tyr Met Val Trp Arg Glu Thr
1439 145      150      155      160
1440 Ile Ser Ser Thr Ala Thr Leu Gly Phe Arg Ile Glu Gly Ile Lys Lys
1441      165      170      175
1442 Ser Asp Gly Lys Ser Ser Lys Asp Phe Lys Thr Thr Lys Asn Arg Asp
1443      180      185      190
1444 Gln Val Ile Glu Ala Phe Arg Asp Phe Val Ala Gly Phe Pro His Val
1445      195      200      205
1446 Ile Pro Lys Tyr Ile Asn Arg Leu Arg Ala Ile Arg Asp Ile Leu Val
1447      210      215      220
1448 Asn Ser Lys Phe Phe Thr Thr His Glu Val Ile Gly Ser Ser Leu Leu
1449 225      230      235      240
1450 Phe Val His Asp Ser Lys Asn Ala Asn Ile Trp Leu Ile Asp Phe Ala

```

↑ Gly Ala Gly Trp Met Asp Asp Ala  
hard return

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
 TIME: 14:44:47

Input Set : A:\seqlist.txt  
 Output Set: N:\CRF3\01272002\J042894.raw

```

1451          245          250          255
1452 Lys Thr Leu Ile Leu Pro Pro Asp Ile Arg Ile Asn His Thr Ser Glu
1453          260          265          270
1454 Trp Val Val Gly Asn His Glu Asp Gly Tyr Leu Ile Gly Ile Asn Asn
1455          275          280          285
E--> 1456
Leu Leu Asp Ile Phe Thr Asp Met Asn Ala Ala Thr Ala Phe Pro Val ↑ 290      295
1494 <210> SEQ ID NO: 29
1495 <211> LENGTH: 21
1496 <212> TYPE: PRT
1497 <213> ORGANISM: Artificial Sequence
1499 <220> FEATURE:
1500 <223> OTHER INFORMATION: consensus sequence
1502 <400> SEQUENCE: 29
E--> 1503
Ile Leu Leu Glu Asn Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu ↑ 5
1505 <210> SEQ ID NO: 30
1506 <211> LENGTH: 33
1507 <212> TYPE: PRT
1508 <213> ORGANISM: Artificial Sequence
1510 <220> FEATURE:
1511 <223> OTHER INFORMATION: consensus sequence
1513 <221> NAME/KEY: VARIANT
1514 <222> LOCATION: (1)...(33)
1515 <223> OTHER INFORMATION: Xaa = Any Amino Acid
1517 <400> SEQUENCE: 30
W--> 1518 Leu Lys Xaa Pro Glu His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly
E--> 1519
1          5          10          15 ↑ Lys Xaa Gly Pro Leu Val Asp Asf
1521 <210> SEQ ID NO: 31
1522 <211> LENGTH: 33
1523 <212> TYPE: PRT
1524 <213> ORGANISM: Artificial Sequence
1526 <220> FEATURE:
1527 <223> OTHER INFORMATION: consensus sequence
1529 <221> NAME/KEY: VARIANT
1530 <222> LOCATION: (1)...(33)
1531 <223> OTHER INFORMATION: Xaa = Any Amino Acid
1533 <400> SEQUENCE: 31
W--> 1534 Leu Lys Xaa Pro Glu His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly
E--> 1535
1          5          10          15 ↑ Lys Xaa Gly Pro Leu Ile Asp Asf
1537 <210> SEQ ID NO: 32
1538 <211> LENGTH: 33
1539 <212> TYPE: PRT
1540 <213> ORGANISM: Artificial Sequence
1542 <220> FEATURE:
1543 <223> OTHER INFORMATION: consensus sequence
1545 <221> NAME/KEY: VARIANT
1546 <222> LOCATION: (1)...(33)
1547 <223> OTHER INFORMATION: Xaa = Any Amino Acid
1549 <400> SEQUENCE: 32
W--> 1550 Leu Lys Xaa Pro Asp His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly

```

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
 TIME: 14:44:47

Input Set : A:\seqlist.txt  
 Output Set : N:\CRF3\01272002\J042894.raw

E--> 1551

1	5	10	15	↑ Lys Xaa Gly Pro Leu Val Asp As
1553	<210>	SEQ ID NO: 33		<i>Same error</i>
1554	<211>	LENGTH: 33		
1555	<212>	TYPE: PRT		
1556	<213>	ORGANISM: Artificial Sequence		
1558	<220>	FEATURE:		
1559	<223>	OTHER INFORMATION: consensus sequence		
1561	<221>	NAME/KEY: VARIANT		
1562	<222>	LOCATION: (1)...(33)		
1563	<223>	OTHER INFORMATION: Xaa = Any Amino Acid		
1565	<400>	SEQUENCE: 33		

W--> 1566 Leu Lys Xaa Pro Asp His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly

E--> 1567

1	5	10	15	↑ Lys Xaa Gly Pro Leu Ile Asp As
1569	<210>	SEQ ID NO: 34		<i>Same</i>
1570	<211>	LENGTH: 41		
1571	<212>	TYPE: PRT		
1572	<213>	ORGANISM: Artificial Sequence		
1574	<220>	FEATURE:		
1575	<223>	OTHER INFORMATION: consensus sequence		
1577	<221>	NAME/KEY: VARIANT		
1578	<222>	LOCATION: (1)...(41)		
1579	<223>	OTHER INFORMATION: Xaa = Any Amino Acid		
1581	<400>	SEQUENCE: 34		

W--> 1582 Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Pro Ser Val Met Asp

E--> 1584

Val	Lys	Xaa	Gly	Ser	Arg	Thr	Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Glu	Xaa	Tyr	↑	20
1586	<210>	SEQ ID NO: 35														<i>Same</i>	
1587	<211>	LENGTH: 41															
1588	<212>	TYPE: PRT															
1589	<213>	ORGANISM: Artificial Sequence															
1591	<220>	FEATURE:															
1592	<223>	OTHER INFORMATION: consensus sequence															
1594	<221>	NAME/KEY: VARIANT															
1595	<222>	LOCATION: (1)...(41)															
1596	<223>	OTHER INFORMATION: Xaa = Any Amino Acid															
1598	<400>	SEQUENCE: 35															

W--> 1599 Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Pro Ser Val Met Asp

E--> 1601

Ile	Lys	Xaa	Gly	Ser	Arg	Thr	Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Glu	Xaa	Tyr	↑	20
1603	<210>	SEQ ID NO: 36														<i>Same</i>	
1604	<211>	LENGTH: 41															
1605	<212>	TYPE: PRT															
1606	<213>	ORGANISM: Artificial Sequence															
1608	<220>	FEATURE:															
1609	<223>	OTHER INFORMATION: consensus sequence															
1611	<221>	NAME/KEY: VARIANT															
1612	<222>	LOCATION: (1)...(41)															
1613	<223>	OTHER INFORMATION: Xaa = Any Amino Acid															
1615	<400>	SEQUENCE: 36															

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002

TIME: 14:44:47

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\01272002\J042894.raw

```
W--> 1616 Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Pro Cys Val Met Asp  
      1617   1           5             10              15  
E--> 1618  
Val Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Glu Xaa Tyr 20
```

See next page for more error

&lt;210&gt; 26

&lt;211&gt; 25

&lt;212&gt; DNA

<213> Artificial Sequence *see item 11 on Ena summary sheet*

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; (1)...(25)

<223> *the numeric identifier and response are mandatory when 2237*

&lt;400&gt; 26

accggttcca ccacgccac tagtc

25 Unknown

*or*  
Artificial Sequence*same ena as seqs. 27-28*

Use of n and/or Xaa has been detected in the Sequence Listing.

Review the Sequence Listing to insure a corresponding explanation is presented in the &lt;220&gt; to &lt;223&gt; fields of each sequence using n or Xaa.

*pkc*

VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
TIME: 14:44:48

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\01272002\J042894.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No  
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:137 M:252 E: No. of Seq. differs, <211>LENGTH:Input:240 Found:224 SEQ:2  
L:248 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:4  
L:248 M:252 E: No. of Seq. differs, <211>LENGTH:Input:227 Found:208 SEQ:4  
L:377 M:252 E: No. of Seq. differs, <211>LENGTH:Input:289 Found:272 SEQ:6  
L:513 M:252 E: No. of Seq. differs, <211>LENGTH:Input:289 Found:272 SEQ:8  
L:639 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:10  
L:639 M:252 E: No. of Seq. differs, <211>LENGTH:Input:279 Found:256 SEQ:10  
L:780 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:12  
L:780 M:252 E: No. of Seq. differs, <211>LENGTH:Input:310 Found:288 SEQ:12  
L:910 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:14  
L:910 M:252 E: No. of Seq. differs, <211>LENGTH:Input:295 Found:272 SEQ:14  
L:980 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:16  
L:980 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:1001 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:17  
L:993 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:997 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1001 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16  
L:1001 M:252 E: No. of Seq. differs, <211>LENGTH:Input:643 Found:480 SEQ:17  
L:1020 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:18  
L:1014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1017 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1019 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1020 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16  
L:1020 M:252 E: No. of Seq. differs, <211>LENGTH:Input:519 Found:360 SEQ:18  
L:1036 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:19  
L:1034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:1036 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16  
L:1036 M:252 E: No. of Seq. differs, <211>LENGTH:Input:353 Found:180 SEQ:19  
L:1148 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:21  
L:1148 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:1248 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22  
L:1299 M:252 E: No. of Seq. differs, <211>LENGTH:Input:322 Found:304 SEQ:23  
L:1456 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:25  
L:1456 M:252 E: No. of Seq. differs, <211>LENGTH:Input:316 Found:288 SEQ:25  
L:1467 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:1479 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:1491 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:1503 M:252 E: No. of Seq. differs, <211>LENGTH:Input:21 Found:0 SEQ:29  
L:1518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:1519 M:252 E: No. of Seq. differs, <211>LENGTH:Input:33 Found:16 SEQ:30  
L:1534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31  
L:1535 M:252 E: No. of Seq. differs, <211>LENGTH:Input:33 Found:16 SEQ:31  
L:1550 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32  
L:1551 M:252 E: No. of Seq. differs, <211>LENGTH:Input:33 Found:16 SEQ:32  
L:1566 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33



VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/042,894

DATE: 01/27/2002  
TIME: 14:44:48

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\01272002\J042894.raw

L:1567 M:252 E: No. of Seq. differs, <211>LENGTH:Input:33 Found:16 SEQ:33  
L:1582 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34  
L:1584 M:252 E: No. of Seq. differs, <211>LENGTH:Input:41 Found:16 SEQ:34  
L:1599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:1601 M:252 E: No. of Seq. differs, <211>LENGTH:Input:41 Found:16 SEQ:35  
L:1616 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36  
L:1618 M:252 E: No. of Seq. differs, <211>LENGTH:Input:41 Found:16 SEQ:36  
L:1633 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1635 M:252 E: No. of Seq. differs, <211>LENGTH:Input:41 Found:16 SEQ:37